AMENDMENTS TO THE SPECIFICATION:

Please delete the paragraph on page 5, lines 8-29 and replace it with the following paragraph:

As already discussed above, a cyclotide is a cyclic peptide which is characterized by being fairly small (the known naturally occurring cyclotides have 28-37 amino acids, although the compounds according to the invention shall not be considered limited to any particular number of amino acids), and by containing six cysteine residues forming three disulphide bridges in a knotted arrangement. A schematic representation of a general cyclotide is given in Formula I:

$C[X_1 \ldots X_a]\ C[X^I_1 \ldots X^I_b]\ C[X^{II}_1 \ldots X^{II}_c]\ C[X^{III}_1 \ldots X^{III}_d]\ C[X^{IV}_1 \ldots X^{IV}_e]\ C[X^V_1 \ldots X^V_f]$

wherein

C is cysteine;

each of $[X_1 \ldots X_a]$, $[X^I_1 \ldots X^I_b]$, $[X^{II}_1 \ldots X^{II}_c]$, $[X^{III}_1 \ldots X^{III}_d]$, $[X^{IV}_1 \ldots X^{IV}_e]$, and $[X^V_1 \ldots X^V_f]$ represents one or more amino acid residues wherein each one or more amino acid residues within or between the sequence residues may be the same or different; and wherein

a, b, c, d, e and f represent the number of amino acid residues in each respective sequence and each of a to f may be the same or different and range from 1 to about 20;

or an analogue of said sequence (SEQ ID NO: 1).

Please delete the paragraph on page 5, line 31 and replace it with the following paragraph:

Preferably each of a to f ranges from 1 to about 10 (SEQ ID NO: 2).

Please delete the paragraph on page 6, lines 1-4 and replace it with the following paragraph:

In a further embodiment a, b, c, d, e and f represent the number of amino acid residues in each respective sequence and wherein a is from about 3 to about 6, b is from about 3 to about 5, c is from about 2 to about 7, d is about 1 to about 3, e is about 3 to about 6, and f is from about 4 to about 9 (SEQ ID NO: 3).

Please delete the paragraph on page 6, lines 6-9 and replace it with the following paragraph:

In a still further embodiment a, b, c, d, e and f represent the number of amino acid residues in each respective sequence and wherein a is about 3, b is about 4, c is from about 4 to about 7, d is about 1, e is about 4 or 5, and f is from about 4 to about 7 (SEQ ID NO: 4).

Please delete the paragraph on page 6, lines 11-13 and replace it with the following paragraph:

Another embodiment is provided wherein a, b, c, d, e and f represent the number of amino acid residues in each respective sequence and wherein a is about 6, b is about 4, c is 3, d is about 1, e is about 5, and f is about 8 (SEQ ID NO: 5).

Please delete the paragraph on page 7, lines 7-19 and replace it with the following paragraph:

The number of cyclotides known to occur in the family of Violaceae, and their high degree of sequence homology, made molecular weight alone insufficient for absolute identification after isolation of the peptide. Hence, it was modified by introduction of charged cleavage sites on the cysteines, followed by enzymatic digestion to produce peptide fragments suitable for sequencing by MS. After aminopropylation and tryptic cleavage the major part of the sequence was obtained. For full coverage, possible cleavage sites were constrained to modified cysteines only: trypsin was exchanged for endoproteinase LysC to prevent cleavage after the arginine residue, native lysine cleavage sites were protected by acetylation, and finally, cysteines were aminoethylated instead of aminopropylated to better suit the chosen enzyme. After this, the full sequence could be determined to cyclo-(VWIPCISSAIGCSCKSKVCYRNGIPCGESC) (SEQ ID NO: 6), unambiguously identifying the peptide as the previously reported cycloviolacin O2.

Please delete the paragraph on page 14, lines 6-14 and replace it with the following paragraph:

After aminopropylation and tryptic cleavage, the sequence of 26 out of 31 amino acids in four identified fragments were successfully determined (sorted after masses, all cysteines converted to their aminopropylated derivatives): VCYR (SEQ ID NO: 7) [597.5 (MH+)] VWIPC (SEQ ID NO: 8) [674.4 (MH+)]; ISSAIGC (SEQ ID NO: 9) [707.5 (MH+)] and NGIPCGESC (SEQ ID NO: 10) [994.5 (MH+)]. The remaining five residues were identified first after acetylation, to protect this particular fragment

from internal cleavage, followed by aminoethylation and tryptic cleavage to KSKVC (SEQ ID NO: 11) [691.3, (MH+)]. Together, these MS data gave the following sequence: cyclo-(VWIPCISSAIGCSCKSKVCYRNGIPCGESC) (SEQ ID NO: 6).